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TECH CENTER 1600/2900

RAW SEQUENCE LISTING

DATE: 04/17/2001

PATENT APPLICATION: US/09/357,273A

TIME: 14:13:36

Input Set : A:\seqlistcorr.txt

Output Set: N:\CRF3\04172001\I357273A.raw

ENTERED

see p.5

3 <110> APPLICANT: Kaufman, Randal J.
 4 Tirasophon, Witoon
 5 Welihinda, Ajith A.
 7 <120> TITLE OF INVENTION: Irelp, A NOVEL MAMMALIAN PROTEIN AND GENE ENCODING SAME
 9 <130> FILE REFERENCE: UMV-1584
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/357,273A
 C--> 12 <141> CURRENT FILING DATE: 1999-07-20
 14 <150> PRIOR APPLICATION NUMBER: 60/093,526
 15 <151> PRIOR FILING DATE: 1998-07-21
 17 <160> NUMBER OF SEQ ID NOS: 14
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 3629
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Artificial Sequence
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (97)..(3027)
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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 36 ccgtaccgcc cccggagcca gggccgagtc ctcgcc atg ccg gcc cgg cgg ctg 114
 37 Met Pro Ala Arg Leu
 38 1 5
 40 ctg ctg ctg ctg acg ctg ctg ctg ccc ggc ctc ggg att ttt gga agt 162
 41 Leu Leu Leu Leu Thr Leu Leu Leu Pro Gly Leu Gly Ile Phe Gly Ser
 42 10 15 20
 44 acc agc aca gtg acg ctt cct gaa acc ttg ttg ttt gtg tca acg ctg 210
 45 Thr Ser Thr Val Thr Leu Pro Glu Thr Leu Leu Phe Val Ser Thr Leu
 46 25 30 35
 48 gat gga agt ttg cat gct gtc agc aag agg aca ggc tca atc aaa tgg 258
 49 Asp Gly Ser Leu His Ala Val Ser Lys Arg Thr Gly Ser Ile Lys Trp
 50 40 45 50
 52 act tta aaa gaa gat cca gtc ctg cag gtc cca aca cat gtg gaa gag 306
 53 Thr Leu Lys Glu Asp Pro Val Leu Gln Val Pro Thr His Val Glu Glu
 54 55 60 65 70
 56 cct gcc ttt ctc cca gat cct aat gat ggc agc ctg tat acg ctt gga 354
 57 Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly Ser Leu Tyr Thr Leu Gly
 58 75 80 85
 60 agc aag aat aat gaa ggc ctg acg aaa ctt cct ttt acc atc cca gaa 402
 61 Ser Lys Asn Asn Glu Gly Leu Thr Lys Leu Pro Phe Thr Ile Pro Glu
 62 90 95 100
 64 ttg gtg cag gca tcc cca tgc cga agt tca gat gga atc ctc tac atg 450
 65 Leu Val Gln Ala Ser Pro Cys Arg Ser Ser Asp Gly Ile Leu Tyr Met
 66 105 110 115
 68 ggt aaa aag cag gac atc tgg tat gtt att gac ctc ctg acc gga gag 498

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69 Gly Lys Lys Gln Asp Ile Trp Tyr Val Ile Asp Leu Leu Thr Gly Glu
70      120      125      130
72 aag cag cag act ttg tca tcg gcc ttt gca gat agt ctc tgc cca tca 546
73 Lys Gln Gln Thr Leu Ser Ser Ala Phe Ala Asp Ser Leu Cys Pro Ser
74 135      140      145      150
76 acc tct ctt ctg tat ctt ggg cga aca gaa tac acc atc acc atg tac 594
77 Thr Ser Leu Leu Tyr Leu Gly Arg Thr Glu Tyr Thr Ile Thr Met Tyr
78      155      160      165
80 gac acc aaa acc cga gag ctc cgg tgg aat gcc acc tac ttt gac tat 642
81 Asp Thr Lys Thr Arg Glu Leu Arg Trp Asn Ala Thr Tyr Phe Asp Tyr
82      170      175      180
84 gcg gcc tca ctg cct gag gac gaa ggg gac tac aag atg tcc cac ttt 690
85 Ala Ala Ser Leu Pro Glu Asp Glu Gly Asp Tyr Lys Met Ser His Phe
86      185      190      195
88 gtg tcc aat ggt gat ggg ctg gtg gtg act gtg gac agt gaa tct ggg 738
89 Val Ser Asn Gly Asp Gly Leu Val Val Thr Val Asp Ser Glu Ser Gly
90      200      205      210
92 gac gtc ctg tgg atc caa aac tac gcc tcc cct gtg gtg gcc ttt tat 786
93 Asp Val Leu Trp Ile Gln Asn Tyr Ala Ser Pro Val Val Ala Phe Tyr
94 215      220      225      230
96 gtc tgg cag cgg gag ggt ctg agg aag gtg atg cac atc aat gtc gct 834
97 Val Trp Gln Arg Glu Gly Leu Arg Lys Val Met His Ile Asn Val Ala
98      235      240      245
100 gtg gag acc ctg cgc tat ctg acc ttc atg tct ggg gag gtg ggg cgc 882
101 Val Glu Thr Leu Arg Tyr Leu Thr Phe Met Ser Gly Glu Val Gly Arg
102      250      255      260
104 atc aca aag tgg aag tac ccg ttc ccc aag gag aca gag gcc aag agc 930
105 Ile Thr Lys Trp Lys Tyr Pro Phe Pro Lys Glu Thr Glu Ala Lys Ser
106      265      270      275
108 aag ctg acg ccc act ctg tat gtt ggg aaa tac tct acc agc ctc tat 978
109 Lys Leu Thr Pro Thr Leu Tyr Val Gly Lys Tyr Ser Thr Ser Leu Tyr
110      280      285      290
112 gcc tct ccc tca atg gta cac gag ggg gtt gct gtc gtg ccc cgc ggc 1026
113 Ala Ser Pro Ser Met Val His Glu Gly Val Ala Val Val Pro Arg Gly
114 295      300      305      310
116 agc aca ctt cct ttg ctg gaa ggg ccc cag act gat ggc gtc acc atc 1074
117 Ser Thr Leu Pro Leu Leu Glu Gly Pro Gln Thr Asp Gly Val Thr Ile
118      315      320      325
120 ggg gac aag ggg gag tgt gtg atc acg ccc agc acg gac gtc aag ttt 1122
121 Gly Asp Lys Gly Glu Cys Val Ile Thr Pro Ser Thr Asp Val Lys Phe
122      330      335      340
124 gat ccc gga ctc aaa agc aag aac aag ctc aac tac ttg agg aat tac 1170
125 Asp Pro Gly Leu Lys Ser Lys Asn Lys Leu Asn Tyr Leu Arg Asn Tyr
126      345      350      355
128 tgg ctt ctg ata gga cac cat gaa acc cca ctg tct gcg tct acc aag 1218
129 Trp Leu Leu Ile Gly His His Glu Thr Pro Leu Ser Ala Ser Thr Lys
130      360      365      370
132 atg ctg gag aga ttt ccc aac aat cta ccc aaa cat cgg gaa aat gtg 1266
133 Met Leu Glu Arg Phe Pro Asn Asn Leu Pro Lys His Arg Glu Asn Val

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134	375		380		385		390	
136	att cct gct gat tca gag aaa aag agc ttt gag gaa gtt atc aac ctg	1314						
137	ile pro ala asp ser glu lys lys ser phe glu glu val ile asn leu							
138			395		400		405	
140	gtt gac cag act tca gaa aac gca cct acc acc gtg tct cgg gat gtg	1362						
141	val asp gln thr ser glu asn ala pro thr thr val ser arg asp val							
142			410		415		420	
144	gag gag aag ccc gcc cat gcc cct gcc cgg ccc gag gcc ccc gtg gac	1410						
145	glu glu lys pro ala his ala pro ala arg pro glu ala pro val asp							
146			425		430		435	
148	tcc atg ctt aag gac atg gct acc atc atc ctg agc acc ttc ctg ctg	1458						
149	ser met leu lys asp met ala thr ile ile leu ser thr phe leu leu							
150			440		445		450	
152	att ggc tgg gtg gcc ttc atc atc acc tat ccc ctg agc atg cat cag	1506						
153	ile gly trp val ala phe ile ile thr tyr pro leu ser met his gln							
154	455		460		465		470	
156	cag cag cag ctc cag cac cag cag ttc cag aag gaa ctg gag aag atc	1554						
157	gln gln gln leu gln his gln gln phe gln lys glu leu glu lys ile							
158			475		480		485	
160	cag ctc ctg cag cag cag cag cag cag ctg ccc ttc cac cca cct gga	1602						
161	gln leu leu gln gln gln gln gln leu pro phe his pro pro gly							
162			490		495		500	
164	gac acg gct cag gac ggc gag ctc ctg gac acg tct ggc ccg tac tca	1650						
165	asp thr ala gln asp gly glu leu leu asp thr ser gly pro tyr ser							
166			505		510		515	
168	gag agc tcg ggc acc agc agc ccc agc acg tcc ccc agg gcc tcc aac	1698						
169	glu ser ser gly thr ser ser pro ser thr ser pro arg ala ser asn							
170			520		525		530	
172	cac tcg ctc tgc tcc ggc agc tct gcc tcc aag gct ggc agc agc ccc	1746						
173	his ser leu cys ser gly ser ser ala ser lys ala gly ser ser pro							
174	535		540		545		550	
176	tcc ctg gaa caa gac gat gga gat gag gaa acc agc gtg gtg ata gtt	1794						
177	ser leu glu gln asp asp gly asp glu glu thr ser val val ile val							
178			555		560		565	
180	ggg aaa att tcc ttc tgt ccc aag gat gtc ctg ggc cat gga gct gag	1842						
181	gly lys ile ser phe cys pro lys asp val leu gly his gly ala glu							
182			570		575		580	
184	ggc aca att gtg tac cgg ggc atg ttt gac aac cgc gac gtg gcc gtg	1890						
185	gly thr ile val tyr arg gly met phe asp asn arg asp val ala val							
186			585		590		595	
188	aag agg atc ctc ccc gag tgt ttt agc ttc gca gac cgt gag gtc cag	1938						
189	lys arg ile leu pro glu cys phe ser phe ala asp arg glu val gln							
190			600		605		610	
192	ctg ttg cga gaa tcg gat gag cac ccg aac gtg atc cgc tac ttc tgc	1986						
193	leu leu arg glu ser asp glu his pro asn val ile arg tyr phe cys							
194	615		620		625		630	
196	acg gag aag gac cgg caa ttc cag tac att gcc atc gag ctg tgt gca	2034						
197	thr glu lys asp arg gln phe gln tyr ile ala ile glu leu cys ala							
198			635		640		645	

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200 gcc acc ctg caa gag tat gtg gag cag aag gac ttt gcg cat ctc ggc 2082
201 Ala Thr Leu Gln Glu Tyr Val Glu Gln Lys Asp Phe Ala His Leu Gly
202      650      655      660
204 ctg gag ccc atc acc ttg ctg cag cag acc acc tcg ggc ctg gcc cac 2130
205 Leu Glu Pro Ile Thr Leu Leu Gln Gln Thr Thr Ser Gly Leu Ala His
206      665      670      675
208 ctc cac tcc ctc aac atc gtt cac aga gac cta aag cca cac aac atc 2178
209 Leu His Ser Leu Asn Ile Val His Arg Asp Leu Lys Pro His Asn Ile
210      680      685      690
212 ctc ata tcc atg ccc aat gca cac ggc aag atc aag gcc atg atc tcc 2226
213 Leu Ile Ser Met Pro Asn Ala His Gly Lys Ile Lys Ala Met Ile Ser
214 695      700      705      710
216 gac ttt ggc ctc tgc aag aag ctg gca gtg ggc aga cac agt ttc agc 2274
217 Asp Phe Gly Leu Cys Lys Lys Leu Ala Val Gly Arg His Ser Phe Ser
218      715      720      725
220 cgc cga tct ggg gtg cct ggc aca gaa ggc tgg atc gct cca gag atg 2322
221 Arg Arg Ser Gly Val Pro Gly Thr Glu Gly Trp Ile Ala Pro Glu Met
222      730      735      740
224 ctg agc gaa gac tgt aag gag aac cct acc tac acg gtg gac atc ttt 2370
225 Leu Ser Glu Asp Cys Lys Glu Asn Pro Thr Tyr Thr Val Asp Ile Phe
226      745      750      755
228 tct gca ggc tgc gtc ttt tac tac gtg gtc tct gag ggc agc cac cct 2418
229 Ser Ala Gly Cys Val Phe Tyr Tyr Val Val Ser Glu Gly Ser His Pro
230      760      765      770
232 ttt ggc aag tcc ctg cag cgg cag gcc aac atc ctc ctg ggt gcc tgc 2466
233 Phe Gly Lys Ser Leu Gln Arg Gln Ala Asn Ile Leu Leu Gly Ala Cys
234 775      780      785      790
236 agc ctt gac tgc ttg cac cca gag aag cac gaa gac gtc att gca cga 2514
237 Ser Leu Asp Cys Leu His Pro Glu Lys His Glu Asp Val Ile Ala Arg
238      795      800      805
240 gaa ttg ata gag aag atg att gcg atg gat cct cag aaa cgc ccc tca 2562
241 Glu Leu Ile Glu Lys Met Ile Ala Met Asp Pro Gln Lys Arg Pro Ser
242      810      815      820
244 gcg aac gac gtg ctc aaa cac ccg ttc ttc tgg agc cta gag aag cag 2610
245 Ala Asn Asp Val Leu Lys His Pro Phe Phe Trp Ser Leu Glu Lys Gln
246      825      830      835
248 ctc cag ttc ttc cag gac gtg agc gac aga ata gaa aag gaa tcc ctg 2658
249 Leu Gln Phe Phe Gln Asp Val Ser Asp Arg Ile Glu Lys Glu Ser Leu
250      840      845      850
252 gat ggc ccg atc gtg aag cag tta gag aga ggc ggg aga gcc gtg gtg 2706
253 Asp Gly Pro Ile Val Lys Gln Leu Glu Arg Gly Gly Arg Ala Val Val
254 855      860      865      870
256 aag atg gac tgg cgg gag aac atc act gac ccc ctc cag aca gac ctg 2754
257 Lys Met Asp Trp Arg Glu Asn Ile Thr Asp Pro Leu Gln Thr Asp Leu
258      875      880      885
260 cgt aaa ttc agg acc tat aaa ggt ggt tct gtc aga gat ctc ctc cga 2802
261 Arg Lys Phe Arg Thr Tyr Lys Gly Gly Ser Val Arg Asp Leu Leu Arg
262      890      895      900
264 gcc atg aga aat aag aag cac cac tac cgg gag ctg cct gca gag gtg 2850

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265 Ala Met Arg Asn Lys Lys His His Tyr Arg Glu Leu Pro Ala Glu Val
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268 cgg gag acg ctg ggg acc ctc ccc gac gac ttc gtg tgc tac ttc acg 2898
269 Arg Glu Thr Leu Gly Thr Leu Pro Asp Asp Phe Val Cys Tyr Phe Thr
270          920          925          930
272 tct cgc ttc ccc cac ctc ctc gca cac acc tac cgg gcc atg gag ctg 2946
273 Ser Arg Phe Pro His Leu Leu Ala His Thr Tyr Arg Ala Met Glu Leu
274 935          940          945          950
276 tgc agc cac gag aga ctc ttc cag ccc tac tac ttc cac gag ccc cca 2994
277 Cys Ser His Glu Arg Leu Phe Gln Pro Tyr Tyr Phe His Glu Pro Pro
278          955          960          965
280 gag ccc cag ccc cca gtg act cca gac gcc ctc /tgagcgaggg cggccccctct 3047
281 Glu Pro Gln Pro Pro Val Thr Pro Asp Ala Leu
282          970          975
284 gttctggtgg cccagctgt gactgagggc ctggtcacca caattagagc ttgatgcctc 3107
286 ccggctttgc agggagacca ggcttcccaa accaagtgcc ttgagctgcc tgctctgcag 3167
288 cccacagagg acagtgtga cccaggaag tgggagaagt ggccctcgt gacctacagg 3227
290 gaactgggaa gatgctggcc ccaaaagcct tacggtcatg atgtctgcaa aggagggcct 3287
292 cagagacagc gcgagtagca cccccagcca tctactggat aaacttgctt cagacttttt 3347
294 aaattcctgc ttaatgtcag tctacaggcc ttccaggaag ggagaggagg gaatcgtaca 3407
296 ttttgcttgc gtgctgggac agctaggctg agatgcacca agtacagcct tcaactggaga 3467
298 ccggaattga gaggtggggg atgctgagga gggggaggac ggagttcaga ggggtgtcgtc 3527
300 ctgcagtatg agatttctca ttgatcacag atgtgccag agtagcccag gtcactgtta 3587
302 actagtgttt ctgcagaggc agcaggagcc agcccgaat tc 3629
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306 <211> LENGTH: 977
307 <212> TYPE: PRT
308 <213> ORGANISM: Artificial Sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
313 <400> SEQUENCE: 2
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315 1 5 10 15
317 Leu Gly Ile Phe Gly Ser Thr Ser Thr Val Thr Leu Pro Glu Thr Leu
318 20 25 30
320 Leu Phe Val Ser Thr Leu Asp Gly Ser Leu His Ala Val Ser Lys Arg
321 35 40 45
323 Thr Gly Ser Ile Lys Trp Thr Leu Lys Glu Asp Pro Val Leu Gln Val
324 50 55 60
326 Pro Thr His Val Glu Glu Pro Ala Phe Leu Pro Asp Pro Asn Asp Gly
327 65 70 75 80
329 Ser Leu Tyr Thr Leu Gly Ser Lys Asn Asn Glu Gly Leu Thr Lys Leu
330 85 90 95
332 Pro Phe Thr Ile Pro Glu Leu Val Gln Ala Ser Pro Cys Arg Ser Ser
333 100 105 110
335 Asp Gly Ile Leu Tyr Met Gly Lys Lys Gln Asp Ile Trp Tyr Val Ile
336 115 120 125
338 Asp Leu Leu Thr Gly Glu Lys Gln Gln Thr Leu Ser Ala Phe Ala
339 130 135 140

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1026 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:1026 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:1026 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8